

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.

529 Rec'd PCT/PTC 13 NOV 2000

SEQUENCE LISTING

<110> SmithKline Beecham Biologicals
Ruelle, Jean-Louis

<120> BASB029 Polynucleotides and Polypeptides
from Neisseria Meningitidis

<130> BM45321

<150> PCT/EP99/03255

<151> 1999-05-07

<150> GB 9810276.7

<151> 1998-05-13

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1785

<212> DNA

<213> Bacteria

<400> 1

atgaacaaaa	tataccgcat	catttggaat	agtgccctca	atgcctgggt	cgccgtatcc	60
gagctcacac	gcaaccacac	caaacgcgcc	tccgcaaccg	tggcgaccgc	cgtattggcg	120
acactgttgt	ttgcaacggt	tcaggcgagt	actaccgatg	acgacgattt	atatttagaa	180
cccgtacaac	gcactgctgt	cgtgttgagc	ttccgttccg	ataaagaagg	cacgggagaa	240
aaagaagtta	cagaagattc	aaattgggga	gtatatattc	acaagaaagg	agtactaaca	300
gccggaacaa	tcaccctcaa	agccggcgac	aacctgaaaa	tcaaacaaaa	caccaatgaa	360
aacaccaatg	ccagtagctt	cacctactcg	ctgaaaaaag	acctcacaga	tctgaccagt	420
gttggaactg	aaaaattatc	gtttagcgca	aacagcaata	aagtcaacat	cacaagcgac	480
accaaaggct	tgaatttcgc	gaaaaaaacg	gctgagacca	acggcgacac	cacggttcat	540
ctgaacggta	tcggttcgac	tttgaccgat	acgctgctga	ataccggagc	gaccacaaac	600
gtaaccaacg	acaacgttac	cgatgacgag	aaaaaacgtg	cggcaagcgt	taaagacgta	660
ttaaacgcag	gctggaacat	taaaggcggt	aaaccgggta	caacagcttc	cgataacggt	720
gatttcgtcc	gcacttacga	cacagtcgag	ttcttgagcg	cagatacgaa	aacaacgact	780
gttaatgtgg	aaagcaaaga	caacggcaag	agaaccgaag	ttaaaatcgg	tgcgaagact	840
tctgttatca	aagaaaaaga	cggtaagttg	gttactggta	aagacaaagg	cgagaatgat	900
tcttctacag	acaaaggcga	aggcttagtg	actgcaaaag	aagtgattga	tgcagtaaac	960
aaggctggtt	ggagaatgaa	aacaacaacc	gctaattggtc	aaacagggtca	agctgacaag	1020
tttgaaacgg	ttacatcagg	cacaaatgta	acctttgcta	gtggtaaagg	tacaactgcg	1080
actgtaagta	aagatgatca	aggcaacatc	actgttatgt	atgatgtaaa	tgtcggcgat	1140
gccctaaacg	tcaatcagct	gcaaaacagc	ggttggaatt	tggattccaa	agcggttgca	1200
ggttcttcgg	gcaaagtcac	cagcggcaat	gtttcgccga	gcaagggaaa	gatggatgaa	1260
accgtcaaca	ttaatgccgg	caacaacatc	gagattaccc	gcaacggcaa	aaatatcgac	1320
atcgccactt	cgatgacccc	gcaattttcc	agcgtttcgc	tcggcgcggg	ggcggatgcg	1380
cccactttaa	gcgtggatga	cgagggcgcg	ttgaatgtcg	gcagcaagga	tgccaacaaa	1440
cccgtccgca	ttaccaatgt	cgccccgggc	gttaaagagg	gggatgttac	aaacgtcgca	1500
caacttaaag	gcgtggcgca	aaacttgaac	aaccacatcg	acaatgtgga	cggcaacgcg	1560
cgtgcgggca	tcgcccgaagc	gattgcaacc	gcaggtctgg	ttcaggcgta	tctgcccggc	1620
aagagtatga	tggcgatcgg	cggcggcact	tatcgcgggc	aagccgggta	tgccatcggc	1680
tactcaagca	tttccgacgg	cggaaattgg	attatcaaag	gcacggcttc	cggcaattcg	1740
cgcggccatt	tcggtgcttc	cgcactctgtc	ggttatcagt	ggtaa		1785

<210> 2

<211> 594

<212> PRT

<213> Bacteria

<400> 2

Met	Asn	Lys	Ile	Tyr	Arg	Ile	Ile	Trp	Asn	Ser	Ala	Leu	Asn	Ala	Trp
1				5					10					15	
Val	Ala	Val	Ser	Glu	Leu	Thr	Arg	Asn	His	Thr	Lys	Arg	Ala	Ser	Ala
			20					25					30		
Thr	Val	Ala	Thr	Ala	Val	Leu	Ala	Thr	Leu	Leu	Phe	Ala	Thr	Val	Gln
		35					40					45			
Ala	Ser	Thr	Thr	Asp	Asp	Asp	Asp	Leu	Tyr	Leu	Glu	Pro	Val	Gln	Arg
	50				55						60				
Thr	Ala	Val	Val	Leu	Ser	Phe	Arg	Ser	Asp	Lys	Glu	Gly	Thr	Gly	Glu
65				70					75						80
Lys	Glu	Val	Thr	Glu	Asp	Ser	Asn	Trp	Gly	Val	Tyr	Phe	Asp	Lys	Lys
				85					90					95	
Gly	Val	Leu	Thr	Ala	Gly	Thr	Ile	Thr	Leu	Lys	Ala	Gly	Asp	Asn	Leu
			100					105					110		
Lys	Ile	Lys	Gln	Asn	Thr	Asn	Glu	Asn	Thr	Asn	Ala	Ser	Ser	Phe	Thr
		115					120					125			
Tyr	Ser	Leu	Lys	Lys	Asp	Leu	Thr	Asp	Leu	Thr	Ser	Val	Gly	Thr	Glu
	130					135						140			
Lys	Leu	Ser	Phe	Ser	Ala	Asn	Ser	Asn	Lys	Val	Asn	Ile	Thr	Ser	Asp
145					150					155					160
Thr	Lys	Gly	Leu	Asn	Phe	Ala	Lys	Lys	Thr	Ala	Glu	Thr	Asn	Gly	Asp
				165					170					175	
Thr	Thr	Val	His	Leu	Asn	Gly	Ile	Gly	Ser	Thr	Leu	Thr	Asp	Thr	Leu
			180					185					190		
Leu	Asn	Thr	Gly	Ala	Thr	Thr	Asn	Val	Thr	Asn	Asp	Asn	Val	Thr	Asp
		195					200					205			
Asp	Glu	Lys	Lys	Arg	Ala	Ala	Ser	Val	Lys	Asp	Val	Leu	Asn	Ala	Gly
	210				215						220				
Trp	Asn	Ile	Lys	Gly	Val	Lys	Pro	Gly	Thr	Thr	Ala	Ser	Asp	Asn	Val
225				230						235					240
Asp	Phe	Val	Arg	Thr	Tyr	Asp	Thr	Val	Glu	Phe	Leu	Ser	Ala	Asp	Thr
			245						250					255	
Lys	Thr	Thr	Thr	Val	Asn	Val	Glu	Ser	Lys	Asp	Asn	Gly	Lys	Arg	Thr
			260					265					270		
Glu	Val	Lys	Ile	Gly	Ala	Lys	Thr	Ser	Val	Ile	Lys	Glu	Lys	Asp	Gly
		275					280					285			
Lys	Leu	Val	Thr	Gly	Lys	Asp	Lys	Gly	Glu	Asn	Asp	Ser	Ser	Thr	Asp
	290					295					300				
Lys	Gly	Glu	Gly	Leu	Val	Thr	Ala	Lys	Glu	Val	Ile	Asp	Ala	Val	Asn
305				310						315					320
Lys	Ala	Gly	Trp	Arg	Met	Lys	Thr	Thr	Thr	Ala	Asn	Gly	Gln	Thr	Gly
				325					330					335	
Gln	Ala	Asp	Lys	Phe	Glu	Thr	Val	Thr	Ser	Gly	Thr	Asn	Val	Thr	Phe
			340					345					350		
Ala	Ser	Gly	Lys	Gly	Thr	Thr	Ala	Thr	Val	Ser	Lys	Asp	Asp	Gln	Gly
		355					360					365			
Asn	Ile	Thr	Val	Met	Tyr	Asp	Val	Asn	Val	Gly	Asp	Ala	Leu	Asn	Val
	370					375					380				
Asn	Gln	Leu	Gln	Asn	Ser	Gly	Trp	Asn	Leu	Asp	Ser	Lys	Ala	Val	Ala
385				390						395					400
Gly	Ser	Ser	Gly	Lys	Val	Ile	Ser	Gly	Asn	Val	Ser	Pro	Ser	Lys	Gly
				405					410					415	
Lys	Met	Asp	Glu	Thr	Val	Asn	Ile	Asn	Ala	Gly	Asn	Asn	Ile	Glu	Ile
			420					425					430		
Thr	Arg	Asn	Gly	Lys	Asn	Ile	Asp	Ile	Ala	Thr	Ser	Met	Thr	Pro	Gln
		435					440					445			
Phe	Ser	Ser	Val	Ser	Leu	Gly	Ala	Gly	Ala	Asp	Ala	Pro	Thr	Leu	Ser
	450					455					460				
Val	Asp	Asp	Glu	Gly	Ala	Leu	Asn	Val	Gly	Ser	Lys	Asp	Ala	Asn	Lys

```

465          470          475          480
Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val
          485          490          495
Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn His
          500          505          510
Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile
          515          520          525
Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met
          530          535          540
Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly
545          550          555          560
Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala
          565          570          575
Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr
          580          585          590
Gln Trp

```

```

<210> 3
<211> 1776
<212> DNA
<213> Bacteria

```

```

<400> 3
atgaacaaaa tataccgcat catttggaat agtgccctca atgcctgggt cgccgtatcc 60
gagctcacac gcaaccacac caaacgcgcc tccgcaaccg tgaagaccgc cgtattggcg 120
acactgttgt ttgcaacggg tcaggcaagt gctaacaatg aagagcaaga agaagattta 180
tatttagacc ccgtacaacg cactgttgcc gtgttgatag tcaattccga taaagaaggc 240
acgggagaaa aagaaaaagt agaagaaaat tcagattggg cagtatatat caacgagaaa 300
ggagtactaa cagccagaga aatcacctc aaagccggcg acaacctgaa aatcaaacia 360
aacggcacaa acttcaccta ctgcgtgaaa aaagacctca cagatctgac cagtgttgga 420
actgaaaaat tatcgttttag cgcaaacggc aataaagtca acatcacaa cgcacacaaa 480
ggcttgaatt ttgcgaaaga aacggctggg acgaacggcg acaccacggg tcacctgaac 540
ggtattgggt cgactttgac cgatacgctg ctgaataacc gagcgaccac aaacgtaacc 600
aacgacaacg ttaccgatga cgagaaaaaa cgtgcggcaa gcgttaaaga cgtattaaac 660
gcaggctgga acattaaagg cgttaaaccg ggtacaacag cttccgataa cgttgatttc 720
gtccgcactt acgacacagt cgagttcttg agcgcagata cgaaaacaa c gactgttaat 780
gtggaagca aagacaacgg caagaaaacc gaagttaaaa tcggtgcgaa gacttctgtt 840
attaaagaaa aagacggtaa gttggttact ggtaaagaca aaggcgagaa tgggttcttct 900
acagacgaag gcgaaggctt agtgactgca aaagaagtga ttgatgcagt aaacaaggct 960
ggttggagaa tgaaaacaac aaccgctaag ggtcaaacag gtcaagctga caagtttgaa 1020
accgttacat caggcacaaa tgtaaccttt gctagtggta aagggtacaac tgcgactgta 1080
agtaaagatg atcaaggcaa catcactgtt atgtatgatg taaatgtcgg cgatgcccta 1140
aacgtcaatc agctgcaaaa cagcgggttg aatttggtat ccaaagcggg tgcaggttct 1200
tcgggcaaa gtcacagcgg caatgttttc ccgagcaagg gaaagatgga tgaaaccgtc 1260
aacattaatg ccggcaacaa catcgagatt acccgcaacg gtaaaaatat cgacatcgcc 1320
acttcgatga ccccgaggtt ttccagcggt tcgctcggcg cgggggcgga tgcgcccact 1380
ttgagcgtgg atggggacgc attgaatgtc ggcagcaaga aggacaacaa acccgcccg 1440
attaccaatg tcgccccggg cgttaaagag ggggatgtta caaacgtcgc acaacttaaa 1500
ggcgtggcgc aaaacttgaa caaccgcac gacaatgtgg acggcaacgc gcgtgcgggc 1560
atcgcccaag cgattgcaac cgcaggtctg gttcaggcgt atttgcccgg caagagtatg 1620
atggcgatcg gcggcgccac ttatcgcggc gaagccgggt acgccatcgg ctactccagt 1680
atttccgacg gcggaatttg gattatcaaa ggcacggctt ccggcaattc gcgcggccat 1740
ttcgggtgctt ccgcatctgt cggttatcag tggtaa 1776

```

```

<210> 4
<211> 591
<212> PRT
<213> Bacteria

```

```

<400> 4
Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp

```

1				5					10					15		
Val	Ala	Val	Ser	Glu	Leu	Thr	Arg	Asn	His	Thr	Lys	Arg	Ala	Ser	Ala	
			20					25					30			
Thr	Val	Lys	Thr	Ala	Val	Leu	Ala	Thr	Leu	Leu	Phe	Ala	Thr	Val	Gln	
		35					40					45				
Ala	Ser	Ala	Asn	Asn	Glu	Glu	Gln	Glu	Glu	Asp	Leu	Tyr	Leu	Asp	Pro	
	50				55						60					
Val	Gln	Arg	Thr	Val	Ala	Val	Leu	Ile	Val	Asn	Ser	Asp	Lys	Glu	Gly	
65				70					75					80		
Thr	Gly	Glu	Lys	Glu	Lys	Val	Glu	Glu	Asn	Ser	Asp	Trp	Ala	Val	Tyr	
			85					90						95		
Phe	Asn	Glu	Lys	Gly	Val	Leu	Thr	Ala	Arg	Glu	Ile	Thr	Leu	Lys	Ala	
			100					105					110			
Gly	Asp	Asn	Leu	Lys	Ile	Lys	Gln	Asn	Gly	Thr	Asn	Phe	Thr	Tyr	Ser	
		115					120					125				
Leu	Lys	Lys	Asp	Leu	Thr	Asp	Leu	Thr	Ser	Val	Gly	Thr	Glu	Lys	Leu	
	130					135					140					
Ser	Phe	Ser	Ala	Asn	Gly	Asn	Lys	Val	Asn	Ile	Thr	Ser	Asp	Thr	Lys	
145				150					155						160	
Gly	Leu	Asn	Phe	Ala	Lys	Glu	Thr	Ala	Gly	Thr	Asn	Gly	Asp	Thr	Thr	
			165					170						175		
Val	His	Leu	Asn	Gly	Ile	Gly	Ser	Thr	Leu	Thr	Asp	Thr	Leu	Leu	Asn	
			180					185					190			
Thr	Gly	Ala	Thr	Thr	Asn	Val	Thr	Asn	Asp	Asn	Val	Thr	Asp	Asp	Glu	
		195					200					205				
Lys	Lys	Arg	Ala	Ala	Ser	Val	Lys	Asp	Val	Leu	Asn	Ala	Gly	Trp	Asn	
	210					215					220					
Ile	Lys	Gly	Val	Lys	Pro	Gly	Thr	Thr	Ala	Ser	Asp	Asn	Val	Asp	Phe	
225				230					235						240	
Val	Arg	Thr	Tyr	Asp	Thr	Val	Glu	Phe	Leu	Ser	Ala	Asp	Thr	Lys	Thr	
			245					250						255		
Thr	Thr	Val	Asn	Val	Glu	Ser	Lys	Asp	Asn	Gly	Lys	Lys	Thr	Glu	Val	
			260					265					270			
Lys	Ile	Gly	Ala	Lys	Thr	Ser	Val	Ile	Lys	Glu	Lys	Asp	Gly	Lys	Leu	
	275						280					285				
Val	Thr	Gly	Lys	Asp	Lys	Gly	Glu	Asn	Gly	Ser	Ser	Thr	Asp	Glu	Gly	
	290					295					300					
Glu	Gly	Leu	Val	Thr	Ala	Lys	Glu	Val	Ile	Asp	Ala	Val	Asn	Lys	Ala	
305				310					315						320	
Gly	Trp	Arg	Met	Lys	Thr	Thr	Thr	Ala	Asn	Gly	Gln	Thr	Gly	Gln	Ala	
			325					330						335		
Asp	Lys	Phe	Glu	Thr	Val	Thr	Ser	Gly	Thr	Asn	Val	Thr	Phe	Ala	Ser	
		340						345					350			
Gly	Lys	Gly	Thr	Thr	Ala	Thr	Val	Ser	Lys	Asp	Asp	Gln	Gly	Asn	Ile	
		355					360					365				
Thr	Val	Met	Tyr	Asp	Val	Asn	Val	Gly	Asp	Ala	Leu	Asn	Val	Asn	Gln	
	370					375					380					
Leu	Gln	Asn	Ser	Gly	Trp	Asn	Leu	Asp	Ser	Lys	Ala	Val	Ala	Gly	Ser	
385				390					395						400	
Ser	Gly	Lys	Val	Ile	Ser	Gly	Asn	Val	Ser	Pro	Ser	Lys	Gly	Lys	Met	
			405					410					415			
Asp	Glu	Thr	Val	Asn	Ile	Asn	Ala	Gly	Asn	Asn	Ile	Glu	Ile	Thr	Arg	
			420					425					430			
Asn	Gly	Lys	Asn	Ile	Asp	Ile	Ala	Thr	Ser	Met	Thr	Pro	Gln	Phe	Ser	
		435					440					445				
Ser	Val	Ser	Leu	Gly	Ala	Gly	Ala	Asp	Ala	Pro	Thr	Leu	Ser	Val	Asp	
	450					455					460					
Gly	Asp	Ala	Leu	Asn	Val	Gly	Ser	Lys	Lys	Asp	Asn	Lys	Pro	Val	Arg	
465				470					475						480	
Ile	Thr	Asn	Val	Ala	Pro	Gly	Val	Lys	Glu	Gly	Asp	Val	Thr	Asn	Val	
			485						490					495		
Ala	Gln	Leu	Lys	Gly	Val	Ala	Gln	Asn	Leu	Asn	Asn	Arg	Ile	Asp	Asn	

			500					505					510				
Val	Asp	Gly	Asn	Ala	Arg	Ala	Gly	Ile	Ala	Gln	Ala	Ile	Ala	Thr	Ala		
		515					520					525					
Gly	Leu	Val	Gln	Ala	Tyr	Leu	Pro	Gly	Lys	Ser	Met	Met	Ala	Ile	Gly		
	530					535					540						
Gly	Gly	Thr	Tyr	Arg	Gly	Glu	Ala	Gly	Tyr	Ala	Ile	Gly	Tyr	Ser	Ser		
545					550					555					560		
Ile	Ser	Asp	Gly	Gly	Asn	Trp	Ile	Ile	Lys	Gly	Thr	Ala	Ser	Gly	Asn		
			565						570					575			
Ser	Arg	Gly	His	Phe	Gly	Ala	Ser	Ala	Ser	Val	Gly	Tyr	Gln	Trp			
			580					585					590				

<210> 5
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 5
 ggggcatatg aacaaaatat accgcatcat ttggaa

36

<210> 6
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 6
 ggggctcgag ccactgataa ccgacagatg cgga

34